



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 136802

TO: Patricia ~~Patten~~ *Leith*  
Location: REM-3D21/3C18  
Art Unit: 1654  
Tuesday, November 02, 2004

Case Serial Number: 09/991293

From: Edward Hart  
Location: Biotech-Chem Library  
REM-1A55  
Phone: 571-272-2512

[edward.hart@uspto.gov](mailto:edward.hart@uspto.gov)

### Search Notes

Examiner Patten,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

STIC-Biotech/ChemLib

136802

**From:** Leith, Patricia  
**Sent:** Tuesday, November 02, 2004 9:29 AM  
**To:** STIC-Biotech/ChemLib  
**Subject:** 09/991,293

Please search SEQ ID No. 1 for 09/991,293.

Thank you!

*Patty Leith*

*US Patent and Trademark Office  
Tech Center 1600  
Biotechnology  
Art Unit 1654  
REM 3D21*

(571) 272-0968



11/2/04  
AA  
DJP



Query Match 100.0%; Score 21; DB 2; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVFV 4  
|||  
Db 39 PVFV 42

RESULT 3  
H98076  
hypothetical protein spr1642 [imported] - Streptococcus pneumoniae (strain R6)  
C:Species: Streptococcus pneumoniae  
C>Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
C:Accession: H98076  
E:Host: H. J. A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E  
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M  
y, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.  
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A:Reference number: A97872; MUID:21423245; PMID:11544234  
A:Accession: H98076  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-51 <KUR>  
A:Cross-references: UNIPROT:Q8CVD3; GB:AE007317; PIDN:AAL00445.1; PID:g15459313; GSPDB:G  
C:Genetics:  
A:Gene: spr1642

Query Match 100.0%; Score 21; DB 2; Length 51;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVFV 4  
|||  
Db 48 PVFV 51

RESULT 4  
C47468  
small membrane protein (symbiotic nitrogen fixation gene cluster) FixQ - Bradyrhizobium  
C:Species: Bradyrhizobium japonicum  
C>Date: 25-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: C47468  
E:Preisig, O.; Anthanatten, D.; Hennecke, H.  
Proc. Natl. Acad. Sci. U.S.A. 90, 3309-3313, 1993  
A:Title: Genes for a microaerobically induced oxidase complex in Bradyrhizobium japonicum  
A:Reference number: A47468; MUID:93234486; PMID:8386371  
A:Contents: 1109pc4  
A:Accession: C47468  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-54 <PRE>  
A:Cross-references: UNIPROT:Q03076; GB:L07487; NID:g1521196; PIDN:AAA26205.1; PID:g152201  
A:Note: sequence extracted from NCBI backbone (NCBI:129655)

Query Match 100.0%; Score 21; DB 2; Length 54;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVFV 4  
|||  
Db 21 PVFV 24

RESULT 5  
AG1943  
hypothetical protein asl1098 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C:Accession: AG1943

R; Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi;  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, I  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AG1943  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-56 <KUR>  
A:Cross-references: UNIPROT:Q8YXW0; GB:BA000019; PIDN:BA73055.1; PID:g17130444; GSPDB:G  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: asl1098

Query Match 100.0%; Score 21; DB 2; Length 56;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVFV 4  
|||  
Db 36 PVFV 39

RESULT 6  
D85682  
unknown protein encoded by prophage CP-933N [imported] - Escherichia coli (strain O157:H  
C:Species: Escherichia coli  
C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: D85682  
E:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lic, A.; Dimailanta, E.; Pocamoussis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: D85682  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-61 <STO>  
A:Cross-references: UNIPROT:Q8X790; GB:AE005174; NID:g12514736; PIDN:AAG55920.1; GSPDB:G  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: Z1820

Query Match 100.0%; Score 21; DB 2; Length 61;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVFV 4  
|||  
Db 42 PVFV 45

RESULT 7  
B59147  
conotoxin Tx5.1 precursor - cone shell (Conus textile)  
C:Species: Conus textile (cloth-of-gold cone)  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 16-Aug-2004  
C:Accession: B59147  
E:Walker, C.S.; Steel, D.; Jacobsen, R.B.; Lirazan, M.B.; Cruz, L.J.; Hooper, D.; Shetti  
J. Biol. Chem. 274, 30664-30671, 1999  
A:Title: The T-superfamily of conotoxins.  
A:Reference number: A59147; MUID:99452958; PMID:10521453  
A:Accession: B59147  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-62 <WAL>  
A:Cross-references: UNIPROT:Q9U700; GB:AF167164; NID:g6103606; PIDN:AAF03684.1; PID:g610  
A:Note: submitted to GenBank, July 1999  
C:Keywords: amidated carboxyl end; toxin; venom  
F;1-22/Domain: signal sequence #status predicted <SIG>  
F;23-49/Domain: propeptide #status predicted <PRO>  
F;50-60/Product: conotoxin tx5 #status predicted <MAT>  
F;50-57,51-58/Disulfide bonds: #status predicted

```

F:60/Modified site: amidated carboxyl end (Gln) (amide in mature form from following gly
Query Match      100.0%; Score 21; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVFV 4
DB 5 PVFV 8

RESULT 8
D59147
conotoxin Gm5.2 precursor - cone shell (Conus gloriamaris)
C:Species: Conus gloriamaris (glory-of-the-sea cone)
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
C:Accession: D59147
R:Walker, C.S.; Steel, D.; Jacobsen, R.B.; Lirazan, M.B.; Cruz, L.J.; Hooper, D.; Shetty,
J. Biol. Chem. 274, 30664-30671, 1999
A:Title: The T-superfamily of conotoxins.
A:Reference number: A59147; MUID:99452958; PMID:10521453
A:Accession: D59147
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-62 <WAL>
A:Cross-references: UNIPROT:Q9U6Z8; GB:AF167166; NID:G6103610; PIDN:AAF03686.1; PID:G610
A:Note: submitted to GenBank, July 1999
C:Keywords: amidated carboxyl end; toxin; venom
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-49/Domain: propeptide #status predicted <PRO>
F:50-60/Product: conotoxin gm5 #status predicted <MAT>
F:51-58,52-59/Disulfide bonds: #status predicted
F:60/Modified site: amidated carboxyl end (Ser) (amide in mature form from following gly

Query Match      100.0%; Score 21; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVFV 4
DB 5 PVFV 8

RESULT 9
F59147
conotoxin P5.1 precursor - cone shell (Conus purpurascens)
N:Contains: conotoxin p5a
C:Species: Conus purpurascens (purple cone)
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
C:Accession: F59147
R:Walker, C.S.; Steel, D.; Jacobsen, R.B.; Lirazan, M.B.; Cruz, L.J.; Hooper, D.; Shetty,
J. Biol. Chem. 274, 30664-30671, 1999
A:Title: The T-superfamily of conotoxins.
A:Reference number: A59147; MUID:99452958; PMID:10521453
A:Accession: F59147
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA; protein
A:Residues: 1-63 <WAL>
A:Cross-references: UNIPROT:Q9U6Z6; GB:AF167168; NID:G6103614; PIDN:AAF03688.1; PID:G610
A:Note: submitted to GenBank, July 1999
C:Keywords: amidated carboxyl end; toxin; venom
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-50/Domain: propeptide #status predicted <PRO>
F:51-62/Product: conotoxin p5a #status experimental
F:52-59,53-60/Disulfide bonds: #status experimental
F:62/Modified site: amidated carboxyl end (Leu) (amide in mature form from following gly

Query Match      100.0%; Score 21; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVFV 4
DB 5 PVFV 8

```

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DB 5 PVFV 8

RESULT 10
C59147
conotoxin Gm5.1 precursor - cone shell (Conus gloriamaris)
C:Species: Conus gloriamaris (glory-of-the-sea cone)
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
C:Accession: C59147
R:Walker, C.S.; Steel, D.; Jacobsen, R.B.; Lirazan, M.B.; Cruz, L.J.; Hooper, D.; Shetty,
J. Biol. Chem. 274, 30664-30671, 1999
A:Title: The T-superfamily of conotoxins.
A:Reference number: A59147; MUID:99452958; PMID:10521453
A:Accession: C59147
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-63 <WAL>
A:Cross-references: UNIPROT:Q9U6Z9; GB:AF167165; NID:G6103608; PIDN:AAF03685.1; PID:G610
A:Note: submitted to GenBank, July 1999
C:Keywords: toxin; venom
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-50/Domain: propeptide #status predicted <PRO>
F:51-63/Product: conotoxin gm5 #status predicted <MAT>
F:52-59,53-60/Disulfide bonds: #status predicted

Query Match      100.0%; Score 21; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVFV 4
DB 5 PVFV 8

RESULT 11
S15630
Proteinase inhibitor Spi2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C:Accession: S15630
R:Ingilis, J.D.; Hill, R.E.
EMBO J. 10, 255-261, 1991
A:Title: The murine Spi-2 proteinase inhibitor locus: a multigene family with a hypervar:
A:Reference number: S15628; MUID:91122031; PMID:1991447
A:Accession: S15630
A:Molecule type: DNA
A:Residues: 1-66 <ING>
A:Cross-references: EMBL:X56822

Query Match      100.0%; Score 21; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVFV 4
DB 33 PVFV 36

RESULT 12
A11844
hypothetical protein asl0305 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: A11844
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: A11844
A:Status: preliminary
A:Molecule type: DNA

```

```
A;Residues: 1-70 <KUR>
A;Cross-references: UNIPROT:Q8VZ28; GB:BA000019; PIDN:BA000019; PID:g17129650; GSPDB:G
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: asl0305

Query Match
Best Local Similarity 100.0%; Score 21; DB 2; Length 70;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVFV 4
Db 36 PVFV 39

RESULT 13
AB1276
hypothetical gene lmo1610 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB1276
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
; Dominguez-Bernal, G.; Duchaud, E.; Duran, L.; Dussurget, O.; Entian, K.D.; Fsihl, H.
D.; Jones, L.W.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkut, G.; Madueno, E.; Maitournam, A.; Ma
ck, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund,
A;Title: Comparative Genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1276
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-72 <GLA>
A;Cross-references: UNIPROT:Q8Y6S3; GB:NC_003210; PIDN:CAC99688.1; PID:g16411046; GSPDB:
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo1610

Query Match
Best Local Similarity 100.0%; Score 21; DB 2; Length 72;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVFV 4
Db 8 PVFV 11

RESULT 14
S04144
ribosomal protein S19 - Yersinia pseudotuberculosis (fragment)
C;Species: Yersinia pseudotuberculosis
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S04144
R;Gross, U.; Chen, J.H.; Kono, D.H.; Lobo, J.G.; Yu, D.T.Y.
Nucleic Acids Res. 17, 3601-3602, 1989
A;Title: High degree of conservation between ribosomal proteins of Yersinia pseudotuber
A;Reference number: S04140; MUID:99263812; PMID:2657663
A;Accession: S04144
A;Molecule type: DNA
A;Residues: 1-74 <GRO>
A;Cross-references: UNIPROT:P11256; EMBL:X14363; MID:g948644; PIDN:CAA32546.1; PID:g48649
C;Genetics:
A;Gene: rpsS
C;Superfamily: ribosomal protein S19/S15
C;Keywords: protein biosynthesis; ribosome

Query Match
Best Local Similarity 100.0%; Score 21; DB 2; Length 74;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVFV 4
Db 59 PVFV 62
```

## RESULT 15

AB1958

hypothetical protein asr1213 [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004

C;Accession: AB1958

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi;

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, I

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AB1958

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-77 &lt;KUR&gt;

A;Cross-references: UNIPROT:Q8YXK0; GB:BA000019; PIDN:BA073170.1; PID:g17130560; GSPDB:G

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: asr1213

Query Match 100.0%; Score 21; DB 2; Length 77;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVFV 4

Db 36 PVFV 39

Search completed: November 2, 2004, 16:16:10

Job time: 18 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 2, 2004, 16:06:52 : Search time 62 Seconds  
(without alignments)  
37.121 Million cell updates/sec

Title: US-09-991-293A-1

Perfect score: 21

Sequence: 1 PVFV 4

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 02.4

1: uniprot\_sprot.4

2: uniprot\_trembl.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	31	Q9X129	Q9X129 thermotoga
2	21	100.0	38	Q61VD2	Q61vd2 zea mays (m
3	21	100.0	38	RAT37125	Rat37125 zea mays
4	21	100.0	38	RAT37134	Rat37134 zea mays
5	21	100.0	39	Q72XB9	Q72xb9 bacillus ce
6	21	100.0	39	AAS44359	Aas44359 bacillus
7	21	100.0	40	Q89RK4	Q89rk4 bradyrhizob
8	21	100.0	42	Q98TS9	Q98ts9 brachydanio
9	21	100.0	45	Q9BPG4	Q9bpg4 conus ventr
10	21	100.0	46	Q7TJT2	Q7tjt2 human herpe
11	21	100.0	46	Q7TJT4	Q7tjt4 human herpe
12	21	100.0	46	Q7TJT7	Q7tjt7 human herpe
13	21	100.0	46	Q7TJT9	Q7tjt9 human herpe
14	21	100.0	46	Q7TJTU1	Q7tjt1 human herpe
15	21	100.0	46	Q7TJTU3	Q7tjt3 human herpe
16	21	100.0	46	Q7TJTU6	Q7tjt6 human herpe
17	21	100.0	46	Q7TJTU8	Q7tjt8 human herpe
18	21	100.0	46	Q7TJTU0	Q7tjt0 human herpe
19	21	100.0	46	Q7TJTU2	Q7tjt2 human herpe
20	21	100.0	46	Q7TJTU4	Q7tjt4 human herpe
21	21	100.0	46	Q7TJTU7	Q7tjt7 human herpe
22	21	100.0	46	Q7TJTU9	Q7tjt9 human herpe
23	21	100.0	46	Q7TJTU2	Q7tjt2 human herpe
24	21	100.0	46	Q7TJTU5	Q7tjt5 human herpe
25	21	100.0	46	Q7TJTU7	Q7tjt7 human herpe
26	21	100.0	46	Q7TJTU9	Q7tjt9 human herpe
27	21	100.0	46	Q7TJTU1	Q7tjt1 human herpe
28	21	100.0	46	Q7TJTU3	Q7tjt3 human herpe
29	21	100.0	46	Q7TJTU5	Q7tjt5 human herpe
30	21	100.0	46	Q7TJTU7	Q7tjt7 human herpe
31	21	100.0	46	Q7TJTU0	Q7tjt0 human herpe

32	21	100.0	46	2	Q7TJY2	Q7tjy2 human herpe
33	21	100.0	46	2	Q7TJY4	Q7tjy4 human herpe
34	21	100.0	46	2	Q7TJY6	Q7tjy6 human herpe
35	21	100.0	46	2	Q7TJY8	Q7tjy8 human herpe
36	21	100.0	46	2	Q7TJZ1	Q7tjz1 human herpe
37	21	100.0	46	2	Q7TJZ3	Q7tjz3 human herpe
38	21	100.0	46	2	Q7TJZ6	Q7tjz6 human herpe
39	21	100.0	46	2	Q7TJZ8	Q7tjz8 human herpe
40	21	100.0	46	2	Q7TJZ8	Q7tjz8 human herpe
41	21	100.0	46	2	Q7TK00	Q7tk00 human herpe
42	21	100.0	46	2	Q7TK02	Q7tk02 human herpe
43	21	100.0	46	2	Q7TK04	Q7tk04 human herpe
44	21	100.0	46	2	Q7TK08	Q7tk08 human herpe
45	21	100.0	46	2	Q7TK10	Q7tk10 human herpe

#### ALIGNMENTS

##### RESULT 1

Q9X129 PRELIMINARY; PRT; 31 AA.  
AC Q9X129;  
DT 01-NOV-1999 (TREMELrel. 12, Created)  
DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)  
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocustNames-TM1671;  
OS Thermotoga maritima.  
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.  
OX NCBI\_TaxID=2336;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MSB8 / DSM 3109 / ATCC 43589;  
RX MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;  
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,  
Raft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,  
RA McDonald L.A., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,  
RA Stewart A.W., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,  
RA Heidelberg J.F., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,  
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;  
RT "Evidence for lateral gene transfer between Archaea and Bacteria from  
RT genome sequence of Thermotoga maritima."  
RL Nature 399:323-329(1999).  
DR EMBL, AB001808; AAD36738.1; --  
DR FIR; E72225; E72225.  
DR TIGR; TM1671; --  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 31 AA; 3434 MW; F1839C57F02ACCBE CRC64;

Query Match 100.0%; Score 21; DB 2; Length 31;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

QY 1 PVFV 4  
|||  
DB 6 PVFV 9

##### RESULT 2

Q61VD2 PRELIMINARY; PRT; 38 AA.  
AC Q61VD2;  
DT 05-JUL-2004 (TREMELrel. 27, Created)  
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)  
DT 01-OCT-2004 (TREMELrel. 28, Last annotation update)  
DE Arginine/serine-rich splicing factor 1 variant 3.  
GN Name=SRP1;  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;

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RN SEQUENCE FROM N.A.
RP Gupta S., Stryker G., Lal S.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY620405; AAT37134.1; -.
DR EMBL; AY616013; AAT37125.1; -.
DR InterPro; IPR000504; RNA_rec_mot.
DR PROSITE; PS0102; RRM; 1.
SQ SEQUENCE 38 AA; 4558 MW; E9F86A981D1AC2F8 CRC64;

Query Match
Best Local Similarity 100.0%; Score 21; DB 2; Length 38;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVFV 4
DB 3 PVFV 6

RESULT 3
AAT37125 PRELIMINARY; PRT; 38 AA.
AC AAT37125;
DT 01-JUN-2004 (TrEMBLrel. 27, Created)
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE Arginine/serine-rich splicing factor 1 variant 3.
GN SRP1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. B73;
RA Gupta S., Stryker G., Lal S.;
RT "Characterization of two novel arginine/serine-rich splicing factors
RT that are differentially spliced in maize.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY616013; AAT37125.1; -.
SQ SEQUENCE 38 AA; 4558 MW; E9F86A981D1AC2F8 CRC64;

Query Match
Best Local Similarity 100.0%; Score 21; DB 2; Length 38;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVFV 4
DB 3 PVFV 6

RESULT 4
AAT37134 PRELIMINARY; PRT; 38 AA.
AC AAT37134;
DT 01-JUN-2004 (TrEMBLrel. 27, Created)
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE Arginine/serine-rich splicing factor 1 variant 3.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. B73;
RA Gupta S., Stryker G., Lal S.;
RT "Characterization of two novel arginine/serine-rich splicing factors
RT that are differentially spliced in maize.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY620405; AAT37134.1; -.

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SQ SEQUENCE 38 AA; 4558 MW; E9F86A981D1AC2F8 CRC64;

Query Match
Best Local Similarity 100.0%; Score 21; DB 2; Length 38;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVFV 4
DB 3 PVFV 6

RESULT 5
Q72XB9 PRELIMINARY; PRT; 39 AA.
ID Q72XB9;
AC Q72XB9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=BCES459;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=222523;
RN [1]
RP SEQUENCE FROM N.A.
RX Rasto D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Nelson W.C., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RL adaptations and a large plasmid related to Bacillus anthracis pXOI.4".
DR EMBL; AB017281; AAS44359.1; -.
DR TIGR; BCE5459; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 39 AA; 4266 MW; A60D332D68AAA02B CRC64;

Query Match
Best Local Similarity 100.0%; Score 21; DB 2; Length 39;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVFV 4
DB 4 PVFV 7

RESULT 6
AAS44359 PRELIMINARY; PRT; 39 AA.
ID AAS44359;
AC AAS44359;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 04-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN BCE5459.
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=222523;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14960714;
RA Rasto D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RL adaptations and a large plasmid related to Bacillus anthracis pXOI.4".
DR EMBL; AB017281; AAS44359.1; -.
DR TIGR; BCE5459; -.
KW Hypothetical protein.
SQ SEQUENCE 39 AA; 4266 MW; A60D332D68AAA02B CRC64;

Query Match
Best Local Similarity 100.0%; Score 21; DB 2; Length 39;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVFV 4  
Db 4 PVFV 7

RESULT 7  
Q89RK4 PRELIMINARY; PRT; 40 AA.

AC Q89RK4; (TREMELrel. 24, Created)  
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)  
DT 01-JUN-2003 (TREMELrel. 25, Last annotation update)  
DE Cbb3 oxidase subunit IV.  
GN Name=fixQ; OrderedLocusNames=bsr2765;  
OS Bradyrhizobium japonicum.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Bradyrhizobiaceae; Bradyrhizobium.  
OX NCBI\_TaxID=375;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=USDA110;  
RX MEDLINE=22484999; PubMed=12597275;  
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,  
RA Sasanoto S., Watanabe A., Iidesawa K., Iriguchi M., Kawashima K.,  
RA Kohara M., Matsumoto M., Shingo S., Tsuruoka H., Wada T., Yamada M.,  
RA Tabata S.;  
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium  
Bradyrhizobium japonicum USDA110.";  
RL DNA Res. 9:189-197(2002).  
DR EMBL; AP005945; BAC48030.1; -.  
DR InterPro; IPR008621; FixQ.  
DR Pfam; PF05545; FixQ; 1.  
KW Complete proteome.  
SQ SEQUENCE 40 AA; 4621 MW; B88371C311475008 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 40;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVFV 4  
Db 7 PVFV 10

RESULT 8  
Q98TS9 PRELIMINARY; PRT; 42 AA.

AC Q98TS9; (TREMELrel. 17, Created)  
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)  
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)  
DE Fibronectin fn2 (Fragment).  
GN Name=fn1;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zhao Q., Colloidi P.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF342953; AAK07664.1; -.  
DR ZFIN; ZDB-GENE-000426-1; fn1.  
FT NON\_TER 1  
SQ SEQUENCE 42 AA; 4706 MW; 149239502EA68314 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 42;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVFV 4  
Db 9 PVFV 12

RESULT 9  
Q9BPG4 PRELIMINARY; PRT; 45 AA.

AC Q9BPG4; (TREMELrel. 17, Created)  
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)  
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)  
DE Conotoxin scaffold IX.  
OS Conus ventricosus (Mediterranean cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=117992;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21105969; PubMed=11158371;  
RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,  
RA Fainzilber M.;  
RT "Mechanisms for evolving hypervariability: the case of conopeptides.";  
RL Mol. Biol. Evol. 18:120-131(2001).  
DR EMBL; AF214963; AAG60393.1; -.  
SQ SEQUENCE 45 AA; 5109 MW; 92BD5215A7971681 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 45;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVFV 4  
Db 5 PVFV 8

RESULT 10  
Q7TJT2 PRELIMINARY; PRT; 46 AA.

AC Q7TJT2; (TREMELrel. 25, Created)  
DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)  
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)  
DE UL3 (Fragment).  
OS Human herpesvirus 1 (HHV-1) (Human herpes simplex virus 1).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Simplexvirus.  
OX NCBI\_TaxID=10298;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bowden R.J.;  
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY240435; AAP38823.1; -.  
DR InterPro; IPR005035; Herpes UL3.  
DR Pfam; PF03369; Herpes UL3; 1.  
FT NON\_TER 1  
SQ SEQUENCE 46 AA; 5291 MW; E22F3405D6983806 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 46;  
Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVFV 4  
Db 20 PVFV 23

RESULT 11  
Q7TJT4 PRELIMINARY; PRT; 46 AA.

Q7TJT4

01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 25, Last annotation update)  
 DE UL3 (Fragment).  
 OS Human herpesvirus 1 (HHV-1) (Human herpes simplex virus 1).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Simplexvirus.  
 OX NCBI\_TaxID=10298;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bowden R.J.;  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY240434; AAP38820.1; -;  
 DR InterPro; IPR005035; Herpes\_UL3.  
 DR Pfam; PF03369; Herpes\_UL3; 1.  
 FT NON TER 1  
 SQ SEQUENCE 46 AA; 5291 MW; E22F3405D6983806 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVFV 4  
 ||||  
 Db 20 PVFV 23

## RESULT 12

Q7TJT7 PRELIMINARY; PRT; 46 AA.  
 AC Q7TJT7;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 25, Last annotation update)  
 DE UL3 (Fragment).  
 OS Human herpesvirus 1 (HHV-1) (Human herpes simplex virus 1).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Simplexvirus.  
 OX NCBI\_TaxID=10298;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bowden R.J.;  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY240433; AAP38817.1; -;  
 DR InterPro; IPR005035; Herpes\_UL3.  
 DR Pfam; PF03369; Herpes\_UL3; 1.  
 FT NON TER 1  
 SQ SEQUENCE 46 AA; 5307 MW; E22F3405CE8F83806 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVFV 4  
 ||||  
 Db 20 PVFV 23

## RESULT 13

Q7TJT9 PRELIMINARY; PRT; 46 AA.  
 AC Q7TJT9;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE UL3 (Fragment).  
 OS Human herpesvirus 1 (HHV-1) (Human herpes simplex virus 1).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Simplexvirus.  
 OX NCBI\_TaxID=10298;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bowden R.J.;

RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY240432; AAP38814.1; -;  
 DR InterPro; IPR005035; Herpes\_UL3.  
 DR Pfam; PF03369; Herpes\_UL3; 1.  
 FT NON TER 1  
 SQ SEQUENCE 46 AA; 5291 MW; E22F3405D6983806 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVFV 4  
 ||||  
 Db 20 PVFV 23

## RESULT 14

Q7TJU1 PRELIMINARY; PRT; 46 AA.  
 AC Q7TJU1;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE UL3 (Fragment).  
 OS Human herpesvirus 1 (HHV-1) (Human herpes simplex virus 1).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Simplexvirus.  
 OX NCBI\_TaxID=10298;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bowden R.J.;  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY240431; AAP38811.1; -;  
 DR InterPro; IPR005035; Herpes\_UL3.  
 DR Pfam; PF03369; Herpes\_UL3; 1.  
 FT NON TER 1  
 SQ SEQUENCE 46 AA; 5291 MW; E22F3405D6983806 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVFV 4  
 ||||  
 Db 20 PVFV 23

## RESULT 15

Q7TJU3 PRELIMINARY; PRT; 46 AA.  
 AC Q7TJU3;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE UL3 (Fragment).  
 OS Human herpesvirus 1 (HHV-1) (Human herpes simplex virus 1).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Simplexvirus.  
 OX NCBI\_TaxID=10298;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bowden R.J.;  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY240430; AAP38808.1; -;  
 DR InterPro; IPR005035; Herpes\_UL3.  
 DR Pfam; PF03369; Herpes\_UL3; 1.  
 FT NON TER 1  
 SQ SEQUENCE 46 AA; 5291 MW; E22F3405D6983806 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVFV 4  
| | |  
Db 20 PVFV 23

Search completed: November 2, 2004, 16:15:47  
Job time : 63 secs

Crush